



SEQUENCE LISTING

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#10

<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
CELLULOLYTICUS

<130> 40170.6US01

<140> 09/917,783

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<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 1

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala
50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala
65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp
130 135 140

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro
 145 150 155 160
 Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro
 165 170 175
 Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val
 180 185 190
 Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser
 195 200 205
 Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu
 210 215 220
 Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met
 225 230 235 240
 Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly
 245 250 255
 Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn
 260 265 270
 Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys
 275 280 285
 Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu
 290 295 300
 Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr
 305 310 315 320
 Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser
 325 330 335
 Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn
 340 345 350
 Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn
 355 360 365
 Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln
 370 375 380
 Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe
 385 390 395 400
 Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu
 405 410 415
 Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser
 420 425 430
 Asp Pro Met Cys Asp Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr
 435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln
 450 455 460
 Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr
 465 470 475 480
 Ser Ser Ser Pro Pro Pro Pro Pro Ser Pro Ser Ala Ser Pro Ser
 485 490 495
 Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser
 500 505 510
 Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
 515 520 525
 Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Pro Ser Pro Ser Pro Ser
 530 535 540
 Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser
 545 550 555 560
 Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Pro Ser
 565 570 575
 Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr
 580 585 590
 Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu
 595 600 605
 Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr
 610 615 620
 Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr
 625 630 635 640
 Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe
 645 650 655
 Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu
 660 665 670
 Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile
 675 680 685
 Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn
 690 695 700
 Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val
 705 710 715 720
 Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly
 725 730 735
 Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
 740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val
 755 760 765
 Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr
 770 775 780
 Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu
 785 790 795 800
 Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala
 805 810 815
 Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn
 820 825 830
 Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Thr Ser Pro Ser
 835 840 845
 Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly
 850 855 860
 Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val
 865 870 875 880
 Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn
 885 890 895
 Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly
 900 905 910
 Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His
 915 920 925
 Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser
 930 935 940
 Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser
 945 950 955 960
 Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr
 965 970 975
 Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser
 980 985 990
 Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr
 995 1000 1005
 Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp
 1010 1015 1020
 Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn
 1025 1030 1035 1040
 Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu
 1045 1050 1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp
 1060 1065 1070
 Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr
 1075 1080 1085
 Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro
 1090 1095 1100
 Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro
 1105 1110 1115 1120
 Thr Ser Ser Pro Ser Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val
 1125 1130 1135
 Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr
 1140 1145 1150
 Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe
 1155 1160 1165
 Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln
 1170 1175 1180
 Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile
 1185 1190 1195 1200
 Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly
 1205 1210 1215
 Thr Asn Ala Ala Pro Thr Leu Ser Cys Thr Ala Ser
 1220 1225

<210> 2

<211> 3687

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 2

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 tccatcgtgc cgctggcgat gcagcatcct gccatcgccg cgacgcacgt cgacaatccc 180
 tatgcgggag cgaccttctt cgtcaaccgg tactgggccc aagaagtaca gagcgaagcg 240
 gcgaaccaga ccaatgccac tctcgcagcg aaaatgcgcg tcgtttccac atattcgacg 300
 gccgtctgga tggaccgcat cgctgcgac aacggcgctca acggcggacc cggcttgacg 360
 acatatctgg acgccgcctt ctcccagcag cagggaacca cccctgaagt cattgagatt 420
 gtcattctacg atctgccggg acgcgactgc gcggcgctcg cctccaacgg cgaactgccc 480
 gctacggcag cagggttgca gacctatgaa acgcagtaca tcgatccgat tgcgagtatc 540
 ctgagcaatc cgaagtactc cagcctgcgg atcgtgacga tcattgagcc ggactcgctg 600
 ccaaacgcgg tcaccaatat gagcattcaa gcgtgtgcaa cggcggtgcc gtattacgag 660
 caaggcatcg agtacgcgct caccgaaattg caccgcatc cgaacgtgta catctacatg 720
 gacgccgccc actccggctg gcttgggtgg cccaataatg ccagcggata cgtacaggaa 780
 gtccagaagg tcctcaacgc gagcatcggg gtcaacggca tcgacggctt cgtcaccaac 840

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acggcgaatt acacgccgtt gaaggagccg ttcattgaccg ccacccagca ggtcggcgga 900
cagccgggtgg agtcggcgaa tttctaccag tggaatcctg acatcgacga agccgactac 960
gcggttgact tgaactcgcg gctcgtcgcc gctggctttc caagcagcat cggcatgctc 1020
atcgacacct tacgcaacgg ttgggggtgg ccgaacgaac caacaggccc gagcaccgcg 1080
accgatgtca acaccttcgt caaccagtcg aagattgacc ttcggcagca ccgcgccctg 1140
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ccgaacgcgc acctcgacgc gtatgtctgg atcaagccgc cgggtgagtc ggacggcaca 1260
agcgtcgga gcgatccgac aactggcaag aagtcggacc ccatgtcgga cccgacgtac 1320
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accagctcgc cgtcgtcgtc ggggtgtggc tgccggggcg cgtatgtggg gaatagtgat 3420
tggggttctg ggtttacggc gacgggtgac gtgacgaata ccgggagccg ggcgacgaac 3480
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gcgttgaccc aatcaggtgc atcgggtgac gcgacgaacc tgagttacaa caacgtgatc 3600
caaccgggtc agtcgaccac ctccgattc aacggaagtt actcaggaac aaacgccgcg 3660
ccgacgtcga gctgcacagc cagctga
3687

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<210> 3

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 3

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
 1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
 20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
 35 40 45

His Pro Ala Ile Ala
 50

<210> 4

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
 GuxA

<400> 4

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn
 1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn
 20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro
 50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr
 65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp
 85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly
 100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu
 115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro
 130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala
 145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys
 165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
 180 185 190
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
 195 200 205
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
 210 215 220
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
 225 230 235 240
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
 245 250 255
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
 260 265 270
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
 275 280 285
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
 290 295 300
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
 305 310 315 320
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
 325 330 335
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
 340 345 350
 Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
 355 360 365
 Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
 370 375 380
 Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
 385 390 395 400
 Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
 405 410 415
 Ala Asn Ala Arg Pro Ala Val
 420

<210> 5

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 5

Val Ser Gly Gly Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro
 1 5 10 15

Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser
 20 25 30

Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
 35 40 45

Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
 50 55 60

Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
 65 70 75 80

Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu
 85 90 95

Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser
 100 105 110

Asp Trp Ser Asn Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn
 115 120 125

Thr Thr Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val
 130 135 140

Leu Val Trp Gly Thr Glu
 145 150

<210> 6

<211> 1043

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
 GuxA

<400> 6

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
 1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
 20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
 35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala
 50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala
 65 70 75 80

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe
 385 390 395 400
 Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu
 405 410 415
 Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser
 420 425 430
 Asp Pro Met Cys Asp Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr
 435 440 445
 Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln
 450 455 460
 Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Val Ser Gly Gly
 465 470 475 480
 Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln
 485 490 495
 Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp
 500 505 510
 Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser
 515 520 525
 Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn
 530 535 540
 Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp
 545 550 555 560
 Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly
 565 570 575
 Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn
 580 585 590
 Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln
 595 600 605
 Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly
 610 615 620
 Thr Glu Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val Thr
 625 630 635 640
 Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr Asp
 645 650 655
 Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val
 660 665 670
 Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly
 675 680 685

Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr
 690 695 700
 Ser Ala Pro Ser Thr Pro Val Asp Cys Thr Pro Gly Pro Asn Gln Asn
 705 710 715 720
 Gly Val Thr Ser Val Gln Asp Gly Glu Tyr Arg Val Gln Thr Asn Glu
 725 730 735
 Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn Thr Ala Thr Gly
 740 745 750
 Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly Thr Gly Gly Ala
 755 760 765
 Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His Trp Gly Asn Cys
 770 775 780
 Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser Gln Ile Gly Ser
 785 790 795 800
 Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser Gly Ala Tyr Asp
 805 810 815
 Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr Thr Thr Gly Gln
 820 825 830
 Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser Arg Gly Gly Val
 835 840 845
 Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr Val Ala Gly His
 850 855 860
 Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp Lys Ile Ile Ser
 865 870 875 880
 Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn Leu Asp Leu Lys
 885 890 895
 Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu Asn Thr Ser Asp
 900 905 910
 Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp Gln Gly Gly Gln
 915 920 925
 Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr Ser Gly Gly Val
 930 935 940
 Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser Gly Phe
 945 950 955 960
 Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr Asn Gly
 965 970 975
 Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr Asn Tyr
 980 985 990

Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala Thr Asn
 995 1000 1005

Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr Phe Gly
 1010 1015 1020

Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu Ser Cys
 1025 1030 1035 1040

Thr Ala Ser

<210> 7

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
 GuxA

<400> 7

Asp Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Asp
 1 5 10 15

Gly Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln
 20 25 30

Cys Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala
 35 40 45

Asn Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile
 50 55 60

Tyr Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met
 65 70 75 80

Pro Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr
 85 90 95

Thr Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr
 100 105 110

Asn Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met
 115 120 125

Ile Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr
 130 135 140

Ala Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly
 145 150 155 160

Gln Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala
 165 170 175

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala
 180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala
 195 200 205

Gly Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe
 210 215 220

Ser Val Ser Val Thr Ser Gly
 225 230

<210> 8
 <211> 101
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Segment of
 GuxA

<400> 8
 Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser
 1 5 10 15
 Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr
 20 25 30
 Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr
 35 40 45
 Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala
 50 55 60
 Thr Asn Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr
 65 70 75 80
 Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu
 85 90 95
 Ser Cys Thr Ala Ser
 100

<210> 9
 <211> 423
 <212> PRT
 <213> Acidothermus cellulolyticus

<400> 9
 Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn
 1 5 10 15
 Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn
 20 25 30
 Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro
 50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr
 65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp
 85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly
 100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu
 115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro
 130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala
 145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys
 165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
 180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
 195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
 210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
 225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
 245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
 260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
 275 280 285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
 290 295 300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
 305 310 315 320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
 325 330 335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
 340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
 355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
 370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
 385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
 405 410 415

Ala Asn Ala Arg Pro Ala Val
 420

<210> 10

<211> 430

<212> PRT

<213> Cellulomonas fimi

<400> 10

Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val
 1 5 10 15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Ala Gly Arg Gln Ser
 20 25 30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro
 35 40 45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp
 50 55 60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys
 65 70 75 80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro
 85 90 95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr
 100 105 110

Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala
 115 120 125

Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr
 130 135 140

Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro
 145 150 155 160

Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala
 165 170 175

Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile
 180 185 190

Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala
 195 200 205
 Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser
 210 215 220
 Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu
 225 230 235 240
 Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg
 245 250 255
 Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr
 260 265 270
 Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser
 275 280 285
 Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn
 290 295 300
 Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp
 305 310 315 320
 Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro
 325 330 335
 Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr
 340 345 350
 Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu
 355 360 365
 Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe
 370 375 380
 Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln
 385 390 395 400
 Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu
 405 410 415
 Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile
 420 425 430
 <210> 11
 <211> 432
 <212> PRT
 <213> Thermobifida fusca
 <400> 11
 Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp
 1 5 10 15
 Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala
 20 25 30

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Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val
 340 345 350

Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly
 355 360 365

Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly
 370 375 380

Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly
 385 390 395 400

Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp
 405 410 415

Phe Ser Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu
 420 425 430

<210> 12

<211> 221

<212> PRT

<213> Acidothermus cellulolyticus

<400> 12

Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg
 1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile
 20 25 30

Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val
 35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys
 50 55 60

His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser
 65 70 75 80

Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn
 85 90 95

Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg
 100 105 110

Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val
 115 120 125

Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly
 130 135 140

Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val
 145 150 155 160

Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly
195 200 205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu
 210 215 220

<210> 14

<211> 228

<212> PRT

<213> Streptomyces lividans

<400> 14

Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp
 1 5 10 15

Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys
 20 25 30

Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn
 35 40 45

Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr
 50 55 60

Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro
 65 70 75 80

Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr
 85 90 95

Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn
 100 105 110

Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile
 115 120 125

Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala
 130 135 140

Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln
 145 150 155 160

Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr
 165 170 175

Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala
 180 185 190

Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly
 195 200 205

Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser
 210 215 220

Val Ser Val Thr
 225